23. A host cell transformed with the vector of claim 22.

24. The host cell of claim 23, wherein the host is a somatic pine embryo.

25. A method for staging plant embryos comprising:

   a) selecting total RNA from at least one embryo of known developmental age;

   b) determining the level of expression of a multiplicity of genes which hybridize to one or more of SEQ ID NOS: 1-327;

   c) correlating the known developmental ages of the embryos from step 1) with the profile of expression measured in step 2);

   d) applying the correlation of step 3) to a sample of embryo RNA from embryos to be staged; and

   e) determining the embryo stage.

26. The method of claim 25, wherein the measurement of gene expression is by RT-PCR.

27. The method of claim 25, wherein the measurement of gene expression is by nucleic acid hybridization.

28. The method of claim 25, wherein the measurement of gene expression is by determining the level of protein expression.

29. The method of claim 28, wherein protein expression is measured by antibody binding.

30. A method for selecting advantageous plant clones comprising:

a) selecting one or more samples of embryonic RNA from multiple clones of plants;

b) determining that at least one sampled clone has an advantageous characteristic;

c) comparing the embryonic levels of expression of genes which hybridize to one or more of SEQ ID NOS: 1-327 in samples from the advantageous clone with expression levels in at least one clone that does not show the advantageous characteristic; and

d) selecting additional clones which show an embryonic gene expression pattern more similar to that of the advantageous clone than to the pattern of at least one clone that does not show the advantageous characteristic.

31. Method of claim 30 where the clones to be sampled or compared are from about the same developmental age.

32. Method of claim 31 where the development age is visually detected.

33. The method of claim 30, wherein the measurement of gene expression is by RT-PCR.

34. The method of claim 30, wherein the measurement of gene expression is by nucleic acid hybridization.

35. The method of claim 30, wherein the measurement of gene expression is by determining the level of protein expression.

36. The method of claim 35, wherein protein expression is measured by antibody binding.

37. A method of determining embryo fitness comprising:

a) creating a relational database with RNA expression values for genes listed in Table I for embryos of known developmental stages;

b) isolating total RNA from embryos of unknown stage development;

c) measuring expression levels of genes identified in Table I from the isolated total RNA; and

d) correlating the database of step 1) with the pattern of expression determined in steps 2) and 3) to assess proper embryo development.

38. The method of claim 37, wherein the measurement of gene expression is by RT-PCR.

39. The method of claim 37, wherein the measurement of gene expression is by nucleic acid hybridization.

40. The method of claim 37, wherein the measurement of gene expression is by determining the level of protein expression.

41. The method of claim 40, wherein protein expression is measured by antibody binding.

42. A method for selecting advantageous growth conditions for embryo development comprising:

a) determining RNA expression profiles for staged embryos under control culture conditions;

b) altering culture conditions;

c) determining RNA expression profiles for staged embryos under altered culture conditions; and

d) correlating culture change to developmental effect in embryo.